

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	682	(untranslated adj1 region) same (DNA) same (remov\$)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:40
L2	740	(untranslated adj1 region or UTR) same (DNA) same (remov\$)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:40
L3	158	I2 and exonuclease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:40
L4	123	I3 and (nuclease or mung)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:53
L5	417	(site-directed adj1 mutagenesis) same (exonuclease)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:54
L6	191	I5 and (nuclease or Mung adj1 bean)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L7	8388	(exonuclease) and (nuclease or Mung adj1 bean)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L8	4742	I7 and mutagenesis	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L9	2863	I8 and removal	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 13:59
L10	276	I9 and UTR	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:27
L11	20	hammond-philip-w.in.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:36
L12	4133	hammond.in.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:36
L13	11	I12 and UTR	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 14:37

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	6689	(cDNA) same (blunt or cohesive)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:42
L2	2	l1 and exonulcease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:43
L3	8205	(cDNA) same (mutagenesis)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:43
L4	1227	l3 and exonuclease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:44
L5	210	l4 and (mung adj1 bean adj1 nuclease)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:52
L6	420	(exonuclease adj1 III) same (mung adj1 bean adj1 nuclease)	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 15:53
L7	340	l6 and cDNA	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:05
L8	284	(deletion adj1 mutations)same cDNA	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:23
L9	2	"6489145".pn.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:27
L10	2	"6337186".pn.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:35
L11	1600	carlsson.in.	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:36
L12	73390	l11 recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:36
L13	9	l11 and recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:38
L14	2	invitro adj1 recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:39
L15	302	in adj1 vitro adj1 recombination	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:40

L16	150	l15 and exonuclease	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:40
L17	24	l16 and mung	US-PGPUB; USPAT; DERWENT	OR	ON	2005/03/08 16:40

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NEWS	6	DEC 01	LISA now available on STN
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NEWS	8	DEC 15	MEDLINE update schedule for December 2004
NEWS	9	DEC 17	ELCOM reloaded; updating to resume; current-awareness alerts (SDIs) affected
NEWS	10	DEC 17	COMPUAB reloaded; updating to resume; current-awareness alerts (SDIs) affected
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NEWS	13	DEC 17	THREE NEW FIELDS ADDED TO IFIPAT/IFIUDB/IFICDB
NEWS	14	DEC 30	EPFULL: New patent full text database to be available on STN
NEWS	15	DEC 30	CAPLUS - PATENT COVERAGE EXPANDED
NEWS	16	JAN 03	No connect-hour charges in EPFULL during January and February 2005
NEWS	17	FEB 25	CA/CAPLUS - Russian Agency for Patents and Trademarks (ROSPATENT) added to list of core patent offices covered
NEWS	18	FEB 10	STN Patent Forums to be held in March 2005
NEWS	19	FEB 16	STN User Update to be held in conjunction with the 229th ACS National Meeting on March 13, 2005
NEWS	20	FEB 28	PATDPAFULL - New display fields provide for legal status data from INPADOC
NEWS	21	FEB 28	BABS - Current-awareness alerts (SDIs) available
NEWS	22	FEB 28	MEDLINE/LMEDLINE reloaded
NEWS	23	MAR 02	GBFULL: New full-text patent database on STN
NEWS	24	MAR 03	REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS	25	MAR 03	MEDLINE file segment of TOXCENTER reloaded
NEWS EXPRESS			JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005
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=> FIL STNGUIDE		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

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COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.06	0.27

FILE 'HOME' ENTERED AT 14:46:38 ON 08 MAR 2005

=> FIL BIOSIS, EMBASE, MEDLINE, LIFESCI, CAPLUS		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.48

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=> s (UTR or untranslated (1a) region) (S) (ORF or open (1a) reading (1a) frame or cDNA)  
 L1 13822 (UTR OR UNTRANSLATED (1A) REGION) (S) (ORF OR OPEN (1A) READING  
 (1A) FRAME OR CDNA)

=> s l1 and (diges?)  
 L2 543 L1 AND (DIGES?)

=> s l2 and exonuclease  
 L3 1 L2 AND EXONUCLEASE

=> d l3

CS Department of Molecular Biology, Okayama University Medical School, Japan.  
SO Biochimica et biophysica acta, (1992 Jul 15) 1131 (3) 287-99.  
Journal code: 0217513. ISSN: 0006-3002.  
CY Netherlands  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals  
OS GENBANK-D13370; GENBANK-D90373; GENBANK-M80475; GENBANK-M80476;  
GENBANK-M80530; GENBANK-M80531; GENBANK-M80532; GENBANK-M80533;  
GENBANK-M91429; GENBANK-M91430  
EM 199208  
ED Entered STN: 19920904  
Last Updated on STN: 20000303  
Entered Medline: 19920820

L5 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN  
AN 2000:133874 CAPLUS  
DN 132:190497  
TI Methods of producing mRNA-protein conjugates and optimizing their  
formation by removing mRNA 3'-untranslated regions  
IN Hammond, Philip W.; Lipovsek, Dasa  
PA Phyllos, Inc., USA  
SO PCT Int. Appl., 52 pp.  
CODEN: PIXXD2  
DT Patent  
LA English  
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000009737	A1	20000224	WO 1999-US18603	19990816
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2334946	AA	20000224	CA 1999-2334946	19990816
	AU 9954883	A1	20000306	AU 1999-54883	19990816
	EP 1105516	A1	20010613	EP 1999-941179	19990816
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	US 6312927	B1	20011106	US 1999-374962	19990816
	JP 2002522091	T2	20020723	JP 2000-565171	19990816
	US 2002160377	A1	20021031	US 2001-910518	20010720
	US 2004086980	A1	20040506	US 2003-646985	20030821
PRAI	US 1998-96818P	P	19980817		
	US 1999-374962	A3	19990816		
	WO 1999-US18603	W	19990816		
	US 2001-910518	B1	20010720		

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN  
AN 1993:423523 CAPLUS  
DN 119:23523  
TI cDNA cloning, sequencing, expression and possible domain structure of  
human APEX **nuclease** homologous to Escherichia coli  
**exonuclease III**  
AU Seki, Shuji; Hatsushika, Masao; Watanabe, Sekiko; Akiyama, Kosuke; Nagao,  
Kazutaka; Tsutsui, Ken  
CS Okayama Univ. Med. Sch., Okayama, Japan  
SO Biochimica et Biophysica Acta (1992), 1131(3), 287-99  
CODEN: BBACAQ; ISSN: 0006-3002  
DT Journal  
LA English

=> file Medline		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	38.70	39.18

FILE 'MEDLINE' ENTERED AT 14:52:29 ON 08 MAR 2005

FILE LAST UPDATED: 5 MAR 2005 (20050305/UP). FILE COVERS 1950 TO DATE.

On December 19, 2004, the 2005 MeSH terms were loaded.

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RLOAD at an arrow prompt (=>). See also:

<http://www.nlm.nih.gov/mesh/>  
[http://www.nlm.nih.gov/pubs/techbull/nd04/nd04\\_mesh.html](http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html)

OLDMEDLINE now back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the  
MeSH 2005 vocabulary.

This file contains CAS Registry Numbers for easy and accurate  
substance identification.

=> E HAMMOND P W/AU 25

E1	6	HAMMOND P S/AU
E2	9	HAMMOND P V/AU
E3	10 -->	HAMMOND P W/AU
E4	2	HAMMOND PAMELA I/AU
E5	1	HAMMOND PAUL A/AU
E6	5	HAMMOND PAULA T/AU
E7	1	HAMMOND PAULINE/AU
E8	3	HAMMOND PETER/AU
E9	6	HAMMOND PHIL/AU
E10	2	HAMMOND PHILIP W/AU
E11	1	HAMMOND PHILLIP S/AU
E12	54	HAMMOND R/AU
E13	24	HAMMOND R A/AU
E14	4	HAMMOND R B/AU
E15	19	HAMMOND R C/AU
E16	2	HAMMOND R D/AU
E17	3	HAMMOND R E/AU
E18	2	HAMMOND R F/AU
E19	2	HAMMOND R G/AU
E20	12	HAMMOND R H/AU
E21	3	HAMMOND R J/AU
E22	7	HAMMOND R K/AU
E23	63	HAMMOND R L/AU
E24	6	HAMMOND R M/AU
E25	10	HAMMOND R P/AU

=> S (E3) AND 1990<=PY<=1998

10 "HAMMOND P W"/AU

3700412 1990<=PY<=1998

L6 5 ("HAMMOND P W"/AU) AND 1990<=PY<=1998

=> DIS L6 1 IBIB ABS

L6 ANSWER 1 OF 5 MEDLINE on STN

ACCESSION NUMBER: 1998215641 MEDLINE

DOCUMENT NUMBER: PubMed ID: 9548747

TITLE: Euplotes telomerase: evidence for limited base-pairing  
during primer elongation and dGTP as an effector of  
translocation.

AUTHOR: Hammond P W; Cech T R

CORPORATE SOURCE: Department of Chemistry and Biochemistry, Howard Hughes  
Medical Institute, University of Colorado, Boulder,  
Colorado 80309-0215, USA.

CONTRACT NUMBER: GM28039 (NIGMS)  
SOURCE: Biochemistry, (1998 Apr 14) 37 (15) 5162-72.  
Journal code: 0370623. ISSN: 0006-2960.

PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199805  
ENTRY DATE: Entered STN: 19980520  
Last Updated on STN: 19980520  
Entered Medline: 19980514

AB The telomeric sequence repeats at the ends of eukaryotic chromosomes are maintained by the ribonucleoprotein enzyme telomerase. Telomeric DNA primers are bound by telomerase both at the active site, which includes base-pairing with the RNA template, and at a second anchor site. The stabilities of Euplotes aediculatus primer-telomerase complexes were determined by measuring their dissociation rates (koff), using an assay involving photo-cross-linking at the anchor site. The primer length was varied, and mismatched substitutions were introduced in a systematic manner. We observed that koff does not scale with primer length as expected for accumulated primer-template base-pairing. This suggests that telomerase maintains a more-or-less constant number of base pairs, similar to the transcription bubble maintained by RNA polymerase. An upper limit was estimated by comparing the experimental koff for the primer-telomerase complex to that of a model DNA-RNA duplex. All the binding energy could be attributed to 10 or 11 base pairs; alternatively, there could be <10 base pairs, with the remaining energy contributed by other parts of telomerase. Most primers exhibited biphasic dissociation kinetics, with variations in both the amount in each phase and the rate for each phase. Since the cross-links monitored in the dissociation assay were all formed with the 5' region of the primer, the two phases may arise from different base-pairing registers with the RNA template, possibly representing pre- and post-translocation complexes. A shift from slow phase to fast phase dissociation was observed in the presence of dGTP, which may implicate dGTP as a positive effector of translocation.

=> DIS L6 2- IBIB ABS

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):Y

L6 ANSWER 2 OF 5 MEDLINE on STN  
ACCESSION NUMBER: 97426515 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 9278493  
TITLE: dGTP-dependent processivity and possible template switching  
of euplotes telomerase.

AUTHOR: Hammond P W; Cech T R  
CORPORATE SOURCE: Department of Chemistry and Biochemistry, Howard Hughes  
Medical Institute, University of Colorado, Boulder, CO  
80309-0215, USA.

CONTRACT NUMBER: GM28039 (NIGMS)  
SOURCE: Nucleic acids research, (1997 Sep 15) 25 (18)  
3698-704.  
Journal code: 0411011. ISSN: 0305-1048.

PUB. COUNTRY: ENGLAND: United Kingdom  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199710  
ENTRY DATE: Entered STN: 19971105  
Last Updated on STN: 19971105  
Entered Medline: 19971017

AB We have measured the processivity of telomeric DNA extension by Euplotes aediculatus telomerase at various concentrations of the nucleotide substrates dGTP and dTTP. The maximum processivity (approximately 3 repeats) was observed at approximately 100 microm of each dNTP.

Processivity decreased as the dNTP concentrations were reduced and, surprisingly, as the concentration of dGTP was increased. Also, the characteristic banding pattern generated by telomerase extension of DNA primers shifted in response to changes in dGTP concentration. One pattern with 8 nt periodicity was predominant at dGTP concentrations  $\leq 16$   $\mu\text{M}$ , while at  $\geq 250$   $\mu\text{M}$  an 8 nt repeat pattern out-of-phase with the first was observed; at intermediate concentrations the two patterns coexisted. We propose that two different segments of the RNA subunit can serve as the template for repeat synthesis; nt 42-49 at low dGTP concentrations and nt 36-43 at high dGTP concentrations. An alternative model for the low dGTP pattern involves an internal pause site but no pause at the end of the template and is, therefore, considered less likely. Because the effects of dGTP on processivity and banding pattern appear to be distinct from nucleotide binding in the polymerase active site, we propose a second dGTP binding site involved in template selection and processivity.

L6 ANSWER 3 OF 5 MEDLINE on STN  
 ACCESSION NUMBER: 97169225 MEDLINE  
 DOCUMENT NUMBER: PubMed ID: 9016672  
 TITLE: Detection of all single-base mismatches in solution by chemiluminescence.  
 AUTHOR: Nelson N C; **Hammond P W**; Matsuda E; Goud A A; Becker M M  
 CORPORATE SOURCE: Gen-Probe Incorporated, San Diego, CA 92121, USA.  
 SOURCE: Nucleic acids research, (1996 Dec 15) 24 (24) 4998-5003.  
 Journal code: 0411011. ISSN: 0305-1048.  
 PUB. COUNTRY: ENGLAND: United Kingdom  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals; AIDS  
 ENTRY MONTH: 199703  
 ENTRY DATE: Entered STN: 19970321  
 Last Updated on STN: 19970321  
 Entered Medline: 19970311

AB A rapid in-solution method for the detection of all 12 single-base mismatches is described. The technique is based on the hybridization protection assay (HPA) format that utilizes oligonucleotide probes labeled with a highly chemiluminescent acridinium ester (AE). Hydrolysis by weak base renders AE permanently non-chemiluminescent. When an AE-labeled probe hybridizes to an exactly complementary target, AE is protected from hydrolysis relative to the unhybridized conformation. Single-base mutations in the duplex adjacent to the site of AE attachment disrupt this protection resulting in rapid AE hydrolysis and loss of chemiluminescence. The discrimination effect was seen in both DNA and RNA. Studies of  $T_m$  values revealed that this effect is not due to a decrease in the overall stability of the duplex, suggesting the AE is responding to local structural changes in the double helix induced by mismatches. Using this principle all 12 single mismatches were clearly discriminated from the corresponding matched sequences. The assay is homogeneous, simple, sensitive, applicable to both amplified and non-amplified targets, and is completed in 30-60 min. An example showing discrimination between wild-type and mutant sequences corresponding to the reverse transcriptase coding region of HIV-1 is given.

L6 ANSWER 4 OF 5 MEDLINE on STN  
 ACCESSION NUMBER: 97127386 MEDLINE  
 DOCUMENT NUMBER: PubMed ID: 8972210  
 TITLE: The anchor site of telomerase from *Euplotes aediculatus* revealed by photo-cross-linking to single- and double-stranded DNA primers.  
 AUTHOR: **Hammond P W**; Lively T N; Cech T R  
 CORPORATE SOURCE: Howard Hughes Medical Institute, Department of Chemistry and Biochemistry, University of Colorado, Boulder 80309-0215, USA.  
 CONTRACT NUMBER: GM28039 (NIGMS)  
 SOURCE: Molecular and cellular biology, (1997 Jan) 17 (1) 296-308.

Journal code: 8109087. ISSN: 0270-7306.

PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199701  
ENTRY DATE: Entered STN: 19970219  
Last Updated on STN: 19970219  
Entered Medline: 19970122

AB Telomerase is a ribonucleoprotein enzyme that adds telomeric sequence repeats to the ends of linear chromosomes. In vitro, telomerase has been observed to add repeats to a DNA oligonucleotide primer in a processive manner, leading to the postulation of a DNA anchor site separate from the catalytic site of the enzyme. We have substituted photoreactive 5-iododeoxypyrimidines into the DNA oligonucleotide primer d(T4G4T4G4T4G2) and, upon irradiation, obtained cross-links with the anchor site of telomerase from *Euplotes aediculatus* nuclear extract. No cross-linking occurred with a primer having the same 5' end and a nontelomeric 3' end. These cross-links were shown to be between the DNA primer and (i) a protein moiety of approximately 130 kDa and (ii) U51-U52 of the telomerase RNA. The cross-linked primer could be extended by telomerase in the presence of [ $\alpha$ -32P]dGTP, thus indicating that the 3' end was bound in the enzyme active site. The locations of the cross-links within the single-stranded primers were 20 to 22 nucleotides upstream of the 3' end, providing a measure of the length of DNA required to span the telomerase active and anchor sites. When the single-stranded primers are aligned with the G-rich strand of a *Euplotes* telomere, the cross-linked nucleotides correspond to the duplex region. Consistent with this finding, a cross-link to telomerase was obtained by substitution of 5-iododeoxycytidine into the CA strand of the duplex region of telomere analogs. We conclude that the anchor site in the approximately 130-kDa protein can bind duplex as well as single-stranded DNA, which may be critical for its function at chromosome ends. Quantitation of the processivity with single-stranded DNA primers and double-stranded primers with 3' tails showed that only 60% of the primer remains bound after each repeat addition.

L6 ANSWER 5 OF 5 MEDLINE on STN  
ACCESSION NUMBER: 91272856 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 2053465  
TITLE: Nucleophilic addition to the 9 position of  
9-phenylcarboxylate-10-methylacridinium protects against  
hydrolysis of the ester.  
AUTHOR: Hammond P W; Wiese W A; Waldrop A A 3rd; Nelson N  
C; Arnold L J Jr  
CORPORATE SOURCE: Gen-Probe Inc., San Diego, CA 92121.  
SOURCE: Journal of bioluminescence and chemiluminescence,  
(1991 Jan-Mar) 6 (1) 35-43.  
Journal code: 8612490. ISSN: 0884-3996.  
PUB. COUNTRY: ENGLAND: United Kingdom  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199107  
ENTRY DATE: Entered STN: 19910811  
Last Updated on STN: 19910811  
Entered Medline: 19910724

AB The chemiluminescent reaction of an acridinium ester (AE) requires addition of peroxide to the 9 position of the acridinium ring. The addition of a hydroxide ion to the 9 position of an acridinium ester to form the carbinol adduct has also been well documented. We have observed a similar addition of other nucleophiles to the acridinium ring to form an acridan adduct. The adduct formed with bisulphite has been particularly well-characterized for rate of formation, rate of reversion, and reaction equilibrium. The formation of an adduct (other than H<sub>2</sub>O<sub>2</sub>) has been demonstrated to decrease significantly the reactivity of the adjacent ester bond to alkaline hydrolysis. The resulting, more stable adduct is very useful when the acridinium ester is used as a label in DNA

probe-based assays. The adduct is highly resistant to hydrolysis under the conditions often desired for DNA probe-based assays (high temperature, elevated pH, extended storage).

=> E LIPOVSEK D/AU 25

E1	5	LIPOVOI V V/AU
E2	1	LIPOVOVA PETRA/AU
E3	4 -->	LIPOVSEK D/AU
E4	3	LIPOVSEK DASA/AU
E5	6	LIPOVSEK M/AU
E6	1	LIPOVSEK P/AU
E7	2	LIPOVSEK S/AU
E8	1	LIPOVSEK SASKA/AU
E9	1	LIPOVSEK V/AU
E10	1	LIPOVSEK VARJA/AU
E11	4	LIPOVSKA A/AU
E12	1	LIPOVSKAIA A I/AU
E13	1	LIPOVSKAIA A V/AU
E14	2	LIPOVSKAIA L A/AU
E15	1	LIPOVSKAIA T A/AU
E16	1	LIPOVSKAIA T K/AU
E17	2	LIPOVSKAIA V V/AU
E18	1	LIPOVSKI DELAPPARENT I/AU
E19	1	LIPOVSKI M/AU
E20	1	LIPOVSKII A S/AU
E21	2	LIPOVSKII B S/AU
E22	2	LIPOVSKII I M/AU
E23	1	LIPOVSKII K A/AU
E24	1	LIPOVSKII M A/AU
E25	1	LIPOVSKII S L/AU

=> S (E3)

L7 4 ("LIPOVSEK D"/AU)

=> DIS L7 1- TI

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):N

=> DIS L7 1- IBIB ABS

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):Y

L7 ANSWER 1 OF 4 MEDLINE on STN  
ACCESSION NUMBER: 1999253497 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 10321580  
TITLE: Hepatitis C virus NS3/4A protease.  
AUTHOR: Kwong A D; Kim J L; Rao G; **Lipovsek D**; Raybuck S  
A  
CORPORATE SOURCE: Vertex Pharmaceuticals, Inc., Cambridge, MA 02139, USA..  
kwong@vpharm.com  
SOURCE: Antiviral research, (1999 Feb) 41 (1) 67-84. Ref: 100  
Journal code: 8109699. ISSN: 0166-3542.  
PUB. COUNTRY: Netherlands  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199907  
ENTRY DATE: Entered STN: 19990816  
Last Updated on STN: 20000303  
Entered Medline: 19990730

AB Despite an urgent medical need, a broadly effective anti-viral therapy for the treatment of infections with hepatitis C viruses (HCVs) has yet to be developed. One of the approaches to anti-HCV drug discovery is the design and development of specific small molecule drugs to inhibit the proteolytic processing of the HCV polyprotein. This proteolytic processing is catalyzed by a chymotrypsin-like serine protease which is located in the N-terminal region of non-structural protein 3 (NS3). This

protease domain forms a tight, non-covalent complex with NS4A, a 54 amino acid activator of NS3 protease. The C-terminal two-thirds of the NS3 protein contain a helicase and a nucleic acid-stimulated nucleoside triphosphatase (NTPase) activities which are probably involved in viral replication. This review will focus on the structure and function of the serine protease activity of NS3/4A and the development of inhibitors of this activity.

L7 ANSWER 2 OF 4 MEDLINE on STN  
ACCESSION NUMBER: 1999193949 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 10096285  
TITLE: Smartbombs and cloaking devices.  
COMMENT: Comment on: Nat Biotechnol. 1999 Mar;17(3):265-70. PubMed ID: 10096294  
AUTHOR: Wagner R W; **Lipovsek D**  
SOURCE: Nature biotechnology, (1999 Mar) 17 (3) 227-8.  
JOURNAL code: 9604648. ISSN: 1087-0156.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Commentary  
News Announcement  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199907  
ENTRY DATE: Entered STN: 19990727  
Last Updated on STN: 19990727  
Entered Medline: 19990712

L7 ANSWER 3 OF 4 MEDLINE on STN  
ACCESSION NUMBER: 1999079747 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 9864043  
TITLE: Hepatitis C virus NS3/4A protease.  
AUTHOR: Kwong A D; Kim J L; Rao G; **Lipovsek D**; Raybuck S  
A  
CORPORATE SOURCE: Vertex Pharmaceuticals, Inc., Cambridge, MA 02139, USA..  
kwong@vpharm.com  
SOURCE: Antiviral research, (1998 Dec) 40 (1-2) 1-18. Ref: 98  
JOURNAL code: 8109699. ISSN: 0166-3542.  
PUB. COUNTRY: Netherlands  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199903  
ENTRY DATE: Entered STN: 19990326  
Last Updated on STN: 20000303  
Entered Medline: 19990318

AB Despite an urgent medical need, a broadly effective anti-viral therapy for the treatment of infections with hepatitis C viruses (HCVs) has yet to be developed. One of the approaches to anti-HCV drug discovery is the design and development of specific small molecule drugs to inhibit the proteolytic processing of the HCV polyprotein. This proteolytic processing is catalyzed by a chymotrypsin-like serine protease which is located in the N-terminal region of non-structural protein 3 (NS3). This protease domain forms a tight, non-covalent complex with NS4A, a 54 amino acid activator of NS3 protease. The C-terminal two-thirds of the NS3 protein contain a helicase and a nucleic acid-stimulated nucleoside triphosphatase (NTPase) activities which are probably involved in viral replication. This review will focus on the structure and function of the serine protease activity of NS3/4A and the development of inhibitors of this activity.

L7 ANSWER 4 OF 4 MEDLINE on STN  
ACCESSION NUMBER: 88006403 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 2820881  
TITLE: Genes for immunodominant protein antigens are highly homologous in Mycobacterium tuberculosis, Mycobacterium africanum, and the vaccine strain Mycobacterium bovis BCG.

AUTHOR: Lu M C; Lien M H; Becker R E; Heine H C; Buggs A M;  
**Lipovsek D**; Gupta R; Robbins P W; Grosskinsky C M;  
Hubbard S C; +  
CORPORATE SOURCE: Department of Biology, Massachusetts Institute of  
Technology, Cambridge 02139.  
CONTRACT NUMBER: AI23545 (NIAID)  
SOURCE: Infection and immunity, (1987 Oct) 55 (10) 2378-82.  
Journal code: 0246127. ISSN: 0019-9567.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 198710  
ENTRY DATE: Entered STN: 19900305  
Last Updated on STN: 19970203  
Entered Medline: 19871028

AB The relatedness of immunodominant protein antigens in Mycobacterium tuberculosis, M. africanum, and M. bovis BCG was investigated by comparing the genes that encode major protein antigens in M. tuberculosis with their counterparts in the other two mycobacteria. Genes encoding homologs of M. tuberculosis major protein antigens were isolated from M. africanum and M. bovis BCG by constructing lambda gt11 recombinant DNA expression libraries and screening them with murine monoclonal antibodies and DNA probes. The antibodies were directed against four major protein antigens of M. tuberculosis with molecular masses of 71, 65, 19, and 14 kilodaltons. The isolated M. africanum and M. bovis BCG DNA clones were mapped with restriction endonucleases, and the maps of the mycobacterial genes were confirmed by Southern analysis of mycobacterial genomic DNA. The restriction maps of DNA containing the four genes in M. tuberculosis, M. africanum, and M. bovis BCG are identical, indicating that the immunodominant proteins that they encode are highly homologous in the three mycobacteria. Thus, the immunity against tuberculosis engendered by M. bovis BCG vaccination could be provided, at least in part, by the immune response to these homologous antigens.